

Sequences producing significant alignments:

Score E
(bits) Value

gi 5771354 dbj BAA83501.1 	Sucrose Transporter [Zea mays]	449	e-124
gi 9624451 gb AAF90181.1 	sucrose transporter [Oryza sativa...]	356	1e-96
gi 7489560 pir T02982	probable sucrose transport protein -...	353	9e-96
gi 7024415 emb CAB75882.1 	sucrose transporter 1 [Hordeum v...]	330	7e-89
gi 20152871 gb AAM13408.1 	sucrose transporter SUT1A [Triti...]	303	8e-81
gi 19548165 gb AAL90455.1 	sucrose transporter SUT1D [Triti...]	301	5e-80
gi 20152873 gb AAM13409.1 	sucrose transporter SUT1B [Triti...]	297	5e-79
gi 15718401 dbj BAB68368.1 	sucrose transporter [Oryza sati...]	252	3e-65
gi 19071641 gb AAL84308.1 	sucrose transporter, 5'-partial ...	238	4e-61
gi 16152148 gb AAL14982.1 	sucrose transporter [Oryza sativ...]	187	1e-45
gi 15217323 gb AAK92667.1 	Putative sucrose transporter [Or...]	157	1e-36
gi 37534172 ref NP_921388.1 	putative sucrose transporter [...]	156	2e-36
gi 29467456 dbj BAC67165.1 	sucrose transporter [Oryza sati...]	137	9e-31
gi 37548736 gb AAN15219.1 	sucrose transporter SUT2 [Oryza ...]	89	4e-16
gi 10119908 gb AAG12987.1 	sucrose transporter-like protein...	88	6e-16
gi 31096339 gb AAP43631.1 	sucrose transporter-like protein...	88	1e-15
gi 29467454 dbj BAC67164.1 	sucrose transporter [Oryza sati...]	85	5e-15

gi 6434831 gb AAF08330.1 	putative sucrose transporter [Vit...	85	5e-15
gi 21063927 gb AAM29153.1 	sucrose transporter 2 [Citrus si...	84	1e-14
gi 31455370 emb CAD58887.1 	sucrose transporter [Plantago m...	80	2e-13
gi 15227049 ref NP_178389.1 	sucrose transporter / sucrose-...	75	7e-12
gi 42570661 ref NP_973404.1 	sucrose transporter / sucrose-...	75	7e-12
gi 14161682 gb AAK54857.1 	sucrose transporter [Oryza sativa]	74	1e-11
gi 14161680 gb AAK54856.1 	sucrose transporter [Oryza sativa]	74	1e-11
gi 7488935 pir T14339	sucrose-proton transport protein - c...	70	2e-10
gi 17447420 gb AAF04295.2 	sucrose transporter 1 [Alonsoa m...	70	2e-10
gi 29467452 dbj BAC67163.1 	sucrose transporter [Oryza sati...	66	3e-09
gi 1076644 pir S48789	sucrose transport protein - common t...	66	3e-09
gi 15219686 ref NP_176830.1 	sucrose transporter, putative ...	64	1e-08
gi 549000 sp Q03411 SUT SPIOL	Sucrose transport protein (Su...	63	4e-08
gi 38327323 gb AAR17700.1 	sucrose transporter [Malus x dom...	62	6e-08
gi 15239921 ref NP_199174.1 	sucrose transporter-related / ...	62	6e-08
gi 20147213 gb AAM10322.1 	Atlg22710/T22J18_12 [Arabidopsis...	58	7e-07
gi 15219938 ref NP_173685.1 	sucrose transporter / sucrose-...	58	7e-07
gi 481131 pir S38196	sucrose transport protein SUC2 - Arab...	58	9e-07
gi 10998390 gb AAG25923.1 	sucrose transporter SUT4 [Solanu...	57	2e-06
gi 9957218 gb AAG09270.1 	sucrose transporter [Lycopersicon...	57	2e-06
gi 15225986 ref NP_179074.1 	sucrose transporter, putative ...	56	3e-06
gi 30349815 emb CAD31122.1 	putative sucrose-H ⁺ symporter [...	56	4e-06
gi 18091781 gb AAL58072.1 	sucrose transporter SUC2 [Brassi...	55	7e-06
gi 9957053 gb AAG09191.1 	sucrose transporter SUT4 [Arabido...	55	1e-05
gi 25344709 pir A86234	hypothetical protein [imported] - A...	55	1e-05
gi 15218362 ref NP_172467.1 	sucrose transporter / sucrose-...	55	1e-05
gi 5823000 gb AAD53000.1 	sucrose-proton symporter [Beta vu...	54	2e-05
gi 1076257 pir S51114	sucrose-proton symporter - beet >gi ...	54	2e-05
gi 7649151 gb AAF65765.1 	sucrose transport protein [Euphor...	53	2e-05
gi 28172870 emb CAD61275.1 	sucrose transporter 4 protein [...	53	2e-05
gi 15239949 ref NP_196235.1 	sucrose transporter, putative ...	53	3e-05
gi 542087 pir JQ2389	sucrose transport protein - potato >g...	53	3e-05
gi 575299 emb CAA57726.1 	sucrose transporter [Lycopersicon...	52	4e-05
gi 1076602 pir S48788	sucrose transport protein - tomato (...	52	4e-05
gi 27447671 gb AAO13696.1 	sucrose transporter [Lycopersico...	52	4e-05
gi 6120115 gb AAF04294.1 	sucrose transporter 1 [Asarina ba...	52	6e-05
gi 4091891 gb AAC99332.1 	sucrose transporter [Apium graveo...	52	6e-05
gi 5230818 gb AAD41024.1 	sucrose transport protein SUT1 [P...	52	6e-05
gi 7024413 emb CAB75881.1 	sucrose transporter 2 [Hordeum v...	52	6e-05
gi 5566434 gb AAD45390.1 	sucrose transporter SUT2A [Apium ...	52	6e-05
gi 33620334 emb CAD91334.1 	sucrose transporter [Glycine max]	52	6e-05
gi 7488866 pir T12198	sucrose transport protein - fava bea...	52	6e-05
gi 27227722 emb CAD29832.1 	sucrose transporter [Viscum alb...	52	7e-05
gi 12038843 emb CAC19689.1 	sucrose/proton symporter [Daucu...	52	7e-05
gi 7488936 pir T14340	sucrose-proton transport protein - c...	52	7e-05
gi 16930709 gb AAL32020.1 	sucrose transporter [Vitis vinif...	52	7e-05
gi 6705993 dbj BAA89458.1 	sucrose transporter protein [Dau...	52	7e-05
gi 1086250 pir S52377	sucrose transport protein SUC1 - com...	51	1e-04
gi 6434833 gb AAF08331.1 	putative sucrose transporter [Vit...	51	1e-04
gi 542020 pir S43142	sucrose transport protein - castor be...	51	1e-04
gi 5640023 gb AAD45932.1 	sucrose transport protein [Betula...	51	1e-04
gi 13186184 emb CAC33492.1 	sucrose carrier [Ricinus communis]	50	2e-04
gi 1086253 pir S38657	sucrose transport protein ptpl - com...	50	2e-04
gi 18091779 gb AAL58071.1 	sucrose transporter SUC1 [Brassi...	50	2e-04
gi 12057172 emb CAC19851.1 	sucrose transporter [Arabidopsis...	50	2e-04
gi 15217602 ref NP_177334.1 	sucrose transporter / sucrose-...	50	2e-04
gi 28143940 gb AAO26335.1 	putative sucrose transporter [Br...	50	2e-04
gi 5882292 gb AAD55269.1 	sucrose transporter [Vitis vinifera]	49	6e-04
gi 35187437 gb AAQ84310.1 	fiber sucrose transporter [Gossy...	49	6e-04
gi 2980887 emb CAA12256.1 	Sucrose carrier [Ricinus communis]	48	8e-04

gi 21063921 gb AAM29150.1	citrus sucrose transporter 1 [Ci...	48	0.001	
gi 15217601 ref NP_177333.1	sucrose transporter / sucrose-...	47	0.001	
gi 28371870 gb AAO38059.1	sucrose transporter SUC1 [Brassi...	46	0.003	
gi 4960089 gb AAD34610.1	sucrose transporter-like protein ...	45	0.008	
gi 6434829 gb AAF08329.1	putative sucrose transporter [Vit...	44	0.011	
gi 12322260 gb AAG51155.1	sucrose-proton symporter, 5' par...	43	0.027	
gi 4586604 dbj BAA76434.1	sucrose transport protein [Cicer...	39	0.51	
gi 26522780 dbj BAC44864.1	hypothetical protein [Glycine max]	38	0.68	
gi 40287430 gb AAR83844.1	glycogen debranching enzyme [Bre...	38	1.2	
gi 30349806 emb CAD30831.1	putative sucrose-H+ symporter [...	36	4.0	
gi 22298694 ref NP_681941.1	permease protein of oligopepti...	36	4.0	
gi 40788373 dbj BAA74844.2	KIAA0821 protein [Homo sapiens]	35	7.1	L
gi 7513937 pir T17138	CL1AA protein - rat >gi 2213659 gb A...	35	7.1	L
gi 38089363 ref XP_134383.4	latrophilin 1 [Mus musculus]	35	7.1	L
gi 41281557 ref NP_055736.2	latrophilin 1; lectomedin-2 [H...	35	7.1	L
gi 28972417 dbj BAC65662.1	mKIAA0821 protein [Mus musculus]	35	7.1	L
gi 22969021 ref ZP_00016596.1	COG0477: Permeases of the ma...	35	7.1	
gi 7513940 pir T17156	CL1BB protein - rat >gi 3695121 gb A...	35	7.1	L
gi 21929099 dbj BAC06134.1	seven transmembrane helix recep...	35	7.1	
gi 12621148 ref NP_075251.1	CL1BA protein [Rattus norvegic...	35	7.1	L
gi 7513938 pir T17145	CL1AB protein - rat >gi 3695117 gb A...	35	7.1	L
gi 23110155 ref ZP_00096317.1	COG1448: Aspartate/tyrosine/...	35	7.1	
gi 14043198 gb AAH07587.1	LPHN1 protein [Homo sapiens]	35	7.1	L

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|5771354|dbj|BAA83501.1| Sucrose Transporter [Zea mays]

Length = 521

Score = 449 bits (1052), Expect = e-124

Identities = 255/684 (37%), Positives = 271/684 (39%), Gaps = 399/684 (58%)

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Query: 42  GQLAELSAGV-----VDHVAPISLG-----MVAGGVQYGW-----LTPYVQT 78
          G+L ELS GV              DHVAPISLG      MVAGGVQYGW      LTPYVQT
Sbjct: 6   GEL-ELSVGVRGTGGAAAAAADHVAPISLGRILILAGMVAGGVQYGWALQSLTTPYVQT 64

Query: 79  LGLG-PIAGDRCTSFMWLC-----VGLYS-----PFILTGCMIIIGAA 115
          LGL  +      TSFMWLC              VGLYS      PFIL GCMLI
Sbjct: 65  LGLSHAL-----TSFMWLCGPIAGLVVQPLVGLYSDRCTARWGRRRPFILIGCMLI----- 115

Query: 116 HGPRWLLDFSMADLCFCSSSTNNWWETCCEAVFLVLPYRAEVETECVAVIV----- 166
                               C+AVIV
Sbjct: 116 -----CLAVIVVGFSSDIGA 130

Query: 167 ---DTKE---L--G---HAAIVY-----NNTVQG-----D---HHGPSA---- 191
          DTKE  L  G   HAAIVY              NNTVQG      D   HHGPSA
Sbjct: 131 ALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFSNNNTVQGPARAMMADLCGHHGPSAANSI 190

Query: 192 -----LGNIL-----KWFPFVGFSSDHCSLYVLGFWPARAMA-ANSIGYSSGL 233
          LGNIL              KWFPF+  ++  C              A  AN      L
Sbjct: 191 FCSWMALGNYSSGSTNNWHKWFPFL-LTNACCE-----ACAN-----L 230

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Query: 234 K TSAFLVAVIFAKEANLKGACLTVTL-----NENLPTTKAGG-----PTGPLALA 278
 K AFLVAV+F L CLTVTL N+NLP TKA G P+GP LA
 Sbjct: 231 K-GAFLVAVVF-----L-VMCLTVTLFFANEVVPYRGNQNLTP-TKANGEVETEPSGP--LA 280

Query: 279 VLK-----MPSVLLVT-----FPFIFYDTHDGDPKLYSNAGFKDLPPAITWLSWW 323
 VLK MPSVLLVT FPFIFYDTD W
 Sbjct: 281 VLKGFKNLPTGMPSVLLVTGLTWLSWFFPFIFYDTD-----W 316

Query: 324 MGREIY-----QISAFNE-----LLLNSVIL-----PMCRKVG----- 352
 MGREIY QISAF+E LLLNS++L PMCRKVG
 Sbjct: 317 MGREIYHGDPKGSNAQISAFDEGVRVGSFGLLLNSIVLGFSSFLIEPMCRKVGPRVWVT 376

Query: 353 --FMVVCVAMA-----SLRDYHGY-----SIKAVCSVGVRVGAFFGGFSSFLIER 393
 FMVVCVAMA SL+DYHGY SIKAVC V L
 Sbjct: 377 SNFMVVCVAMAATALISFWSLKDYGIVQDAITASTSIKAVCLV-----L--- 420

Query: 394 VVWVTSNISFWITANAFLGVPTAQLAATALVQDAVLFA-PFAV-----GLCTG 440
 F AFLGVP L A+L++ PFAV GLCTG
 Sbjct: 421 -----F-----AFLGVP---L-----AILYSVPFAVTAQLAATKGGGQGLCTG 455

Query: 441 VLNIATRGGGQSIVIPQVIAL-----NIPAF-----VVGVFVAVSAG 477
 VLNI SIVIPQVIAL NIPAF VVGVF
 Sbjct: 456 VLNI-----SIVIPQVIALGAGPWDALFGKGNIPAFGVASGFALIGGVVGVF----- 503

Query: 478 GGVASALLPKIGHFALVGSKRQFR 501
 LLPKI SKRQFR
 Sbjct: 504 -----LLPKI-----SKRQFR 514

Score = 71.0 bits (160), Expect = 1e-10

Identities = 41/105 (39%), Positives = 41/105 (39%), Gaps = 64/105 (60%)

Query: 1 MARGDG-----RG-----AAA--V-----RLILAG-----ALQLSL--- 24
 MARGDG RG AAA V RLILAG ALQLSL
 Sbjct: 1 MARGDGELELSVGVRGTGGAAAAAADHVAPISLGRILLAGMVAGGVQYGWALQLSLLTP 60

Query: 25 -----SHALTS-----VVQPL-----RWGRRR 41
 SHALTS VVQPL RWGRRR
 Sbjct: 61 YVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLYSDRCTARWGRRR 105

☐ >gi|9624451|gb|AAF90181.1| sucrose transporter [Oryza sativa (indica cultivar-gr
 Length = 538

Score = 356 bits (833), Expect = 1e-96

Identities = 231/695 (33%), Positives = 254/695 (36%), Gaps = 422/695 (60%)

Query: 46 ELSAGV-----VDHVAPISLG-----MVAGGVQYGW-----LTPYV 76
 ELS GV V+ APISLG MVAGGVQYGW LTPYV
 Sbjct: 19 ELSVGVGGGGGARGGGGGGAAAAVETAAPISLGRILSGMVAGGVQYGWALQLSLLTPYV 78

Query: 77 QTLGLG-PIAGDRCTSEFMWLC-----VGLYS-----PFILTGCMLIIG 113
 QTLGL + TSEFMWLC VGLYS P+ILTGC+LI
 Sbjct: 79 QTLGLSHAL-----TSEFMWLCGPIAGMVVQPCVGLYSDRCTSKWGRRRPYILTGCCLI-- 131

Query: 114 AAHGPRWLLDFSMADLCFCSSTNNWWETCCEAVFLVLPYRAEVETECVAVIV----- 166
 C+AV+V

Sbjct: 132 -----CLAVVVIGFSADI 144

Query: 167 -----DTKE-----LG---HAAIVYNNTVQGDHGPSALGNILKWFPFVGFSDDHCSLYV 213
DTKE G HAAIVY V

Sbjct: 145 GYAMGDTKEEDCSVYHGSRWHAIVY-----V 170

Query: 214 LGFW-----PARA-MA-----ANSI-----GYSSG----- 232
LGFW PARA MA ANSI GYSSG

Sbjct: 171 LGFWLLDFSNNTVQGPALMADLSGRHGPGTANSIFCSWMAMGNILGYSSGSTNNWHKW 230

Query: 233 ---LKT-----SAFLVAVIFAKEANLKGACLTVTL-----NENLPTTKA 268
LKT AFLVAVIF +L CL +TL N LPT K+

Sbjct: 231 FPFLKTRACCEACANLKGAFVAVIFL---SL---CLVITLIFAKEVPFKGNAALPT-KS 283

Query: 269 GGP-----TGPLALAVLK-----MPSVLLVTFPFILYDTHGDPKLYSNAGFKDLPP 315
P TGPLA VLK MPSVL+VT

Sbjct: 284 NEPAEPEGTGPLA--VLKGFRNLPTGMPSVLIVT----- 315

Query: 316 AITWLSW-----WMGREIY-----QISAFNE-----LLLNSVIL----- 344
+TWLSW WMGREIY QI AFN+ LLLNS++L

Sbjct: 316 GLTWLSWFPFILIYDTHWMGREIYHGDPKGTDQIEAFNQGVRAFAFGLLLNSIVLGFSSF 375

Query: 345 ---PMCRKVGP-----FMVCVAMA-----SLRDYHGY-----SIKAVCSV 376
PMCRKVGP F+VC+AMA SL+D+HG SIKAVC V

Sbjct: 376 LIEPMCRKVGPVWVWTSNLFVCIAMAATALISFWSLKDFHGTQKAITADKSIKAVCLV 435

Query: 377 GVRVGAFGGFSSFLIERVVWVTSNISFWITANAFGLGVPTAQLAATALVQDAVLFA-PFAV 435
L F AFLGVP L AVL++ PFAV

Sbjct: 436 -----L-----F-----AFLGVP---L-----AVLYSVPEAV 454

Query: 436 -----GLCTGVLNIATRGGGQSIVIPQVIAL-----NIPAFVVG 471
GLCTGVLNI SIVIPQV+IAL NIPAF G+

Sbjct: 455 TAQLAATRGGGQGLCTGVLNI-----SIVIPQVVIALGAGPWDELFGKGNIPAF--GL 505

Query: 472 ---FA-VSAGGGVASA-LLPKIGHFALVGSKRQFR 501
FA + GGVA LLPKI SKRQFR

Sbjct: 506 ASGFALI---GGVAGIFLLPKI-----SKRQFR 530

Score = 84.6 bits (192), Expect = 8e-15

Identities = 78/285 (27%), Positives = 83/285 (29%), Gaps = 195/285 (68%)

Query: 2 ARGDGRG--AAAV-----RLILAG-----ALQLSL-----SHALTS 30
ARG G G AAV RLIL+G ALQLSL SHALTS

Sbjct: 30 ARGGGGGEAAAVETAAPISLGRILSGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTS 89

Query: 31 -----VVQP---L-----RWGRRRGQLAELSAGVVDHVAPISLGMVAGGVQY 69
VVQP L +WGRRR

Sbjct: 90 FMWLCGPIAGMVVQPCVGLYSDRCTSKWGRRR----- 121

Query: 70 GWLTPYVQTLGLGPIAGDRCTSFMWLCVGLYSPFILTGCMLI-----IGAA-- 115
PY+ LTGC+LI IG A

Sbjct: 122 ----PYI-----LTGCVLICLAVVVIGFSADIGYAMG 149

Query: 116 -----HGPR-----WLLDFS-----MADLC-----FCS 133
HG R WLLDFS MADL FCS

Sbjct: 150 DTKEDCSVYHGSRWHAIVYVLGFWLLDFSNNTVQGPALMADLSGRHGPGTANSIFCS 209

Query: 134 -----STNNW--W----ET--CCEA-----VFLVLV 151

STNNW W +T CCEA FLV V
 Sbjct: 210 WMAMGNILGYSSGSTNNWHKWFPLKTRACCEACANLKGAFVLAV 254

□>gi|7489560|pir||T02982 probable sucrose transport protein - rice
 gi|2723471|dbj|BAA24071.1| sucrose transporter [Oryza sativa (japonica cultivar-g
 Length = 537

Score = 353 bits (826), Expect = 9e-96
 Identities = 230/693 (33%), Positives = 253/693 (36%), Gaps = 421/693 (60%)

Query: 46 ELSAGV-----VDHVAPISLG-----MVAGGVQYGW-----LTPYVQ 77
 ELS GV V+ APISLG MVAGGVQYGW LTPYVQ
 Sbjct: 19 ELSVGVGGGGARGGGGGGAAAAVETAAPISLGRILSGMVAGGVQYGWALQLSLTPYVQ 78

Query: 78 TLGLG-PIAGDRCTSEFMWLC-----VGLYS-----PFILTGCMIIIGA 114
 TLGL + TSFMWLC VGLYS P+ILTGC+LI
 Sbjct: 79 TLGLSHAL-----TSFMWLCGPIAGMVVQPCVGLYSDRCTSKWGRRRPYILTGCVLI--- 130

Query: 115 AHGPRWLLDFSMADLCFCSSSTNNWWETCCEAVFLVLPYRAEVETECVAVIV----- 166
 C+AV+V
 Sbjct: 131 -----CLAVVVIGFSADIG 144

Query: 167 ----DTKE-----LG---HAAIVYNNTVQGDHGHGPSALGNILKWFPFVGFSDDHCSLYVL 214
 DTKE G HAAIVY VL
 Sbjct: 145 YAMGDTKEDCSVYHGSRWHAAIVY-----VL 170

Query: 215 GFW-----PARA-MA-----ANSI-----GYSSG----- 232
 GFW PARA MA ANSI GYSSG
 Sbjct: 171 GFWLLDFSNNTVQGPALALMADLSGRHGP GTANSIFCSWMAMGNILGYSSGSTNNWHKWF 230

Query: 233 --LKT-----SAFLVAVIFAKEANLKGACLTVTL-----NENLPTTKAG 269
 LKT AFLVAVIF +L CL +TL N LPT K+
 Sbjct: 231 PFLKTRACCEACANLKGAFVLVAVIFL---SL---CLVITLIFAKEVPFKGNAALPT-KSN 283

Query: 270 GP-----TGPLALAVLK-----MPSVLLVTFFPFIYDTHGDPKLYSNAGFKDLPPA 316
 P TGPLA VLK MPSVL+VT
 Sbjct: 284 EPAPEGTGPLA--VLKGFRNLPTGMPSVLIVT-----G 315

Query: 317 ITWLSW-----WMGREIY-----QISAFNE-----LLNSVIL----- 344
 +TWLSW WMGREIY QI AFN+ LLNS++L
 Sbjct: 316 LTWLSWFPFIYDTHGDMGREIYHGD PKGTD PQIEAFNQGV RAGAFGLLLNSIVLGFSSFL 375

Query: 345 --PMCRKVGP-----FMVCVAMA-----SLRDYHGY-----SIKAVCSVG 377
 PMCRKVGP F+VC+AMA SL+D+HG SIKAVC V
 Sbjct: 376 IEPMCRKVGP RVVWVTSNFLVCIAMAATALISFWSLKDFHGT VQKAITADKSIKAVCLV- 434

Query: 378 VRVGAFGGFSSFLIERVVWVTSNISFWITANAFLGVPTAQLAATALVQDAVLFA-PFAV- 435
 L F AFLGV L AVL++ PFAV
 Sbjct: 435 -----L-----F-----AFLGV---L-----AVLYSV PFAVT 454

Query: 436 -----GLCTGVLNIATRGGGQSIVIPQVIAL-----NIPAFVVG- 471
 GLCTGVLNI SIVIPQV+IAL NIPAF G+
 Sbjct: 455 AQLAATRGGGQGLCTGVLNI-----SIVIPQVVIALGAGPWDELFGKGNIPAF--GLA 505

Query: 472 --FA-VSAGGGVASA-LLPKIGHFALVGSKRQF 500
 FA + GGVA LLPKI SKRQF
 Sbjct: 506 SGFALI---GGVAGIFLLPKI-----SKRQF 528

Score = 84.6 bits (192), Expect = 8e-15

Identities = 78/285 (27%), Positives = 83/285 (29%), Gaps = 195/285 (68%)

Query: 2 ARGDGRG--AAAV-----RLILAG-----ALQLSL-----SHALTS 30
 ARG G G AA AV RLIL+G ALQLSL SHALTS
 Sbjct: 29 ARGGGGGEAAAVETAAPISLGRILISGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTS 88

Query: 31 -----VVQP---L-----RWGRRRGQLAELSAGVVDHVAPISLGMVAGGVQY 69
 VVQP L +WGRRR
 Sbjct: 89 FMWLCGPIAGMVVQPCVGLYSDRCTSKWGRRR----- 120

Query: 70 GWLTPYVQTLGLGPIAGDRCTSFMWLCVGLYSPFILTGCMLI-----IGAA-- 115
 PY+ LTGC+LI IG A
 Sbjct: 121 ----PYI-----LTGCVLICLAVVIGFSADIGYAMG 148

Query: 116 -----HGPR-----WLLDFS-----MADLC-----FCS 133
 HG R WLLDFS MADL FCS
 Sbjct: 149 DTKEDCSVYHGSRWHAAIVYVLGFWLLDFSNNNTVQGPALMADLSGRHGPGTANSIFCS 208

Query: 134 -----STNNW--W----ET--CCEA-----VFLVLV 151
 STNNW W +T CCEA FLV V
 Sbjct: 209 WMAMGNILGYSSGSTNNWHKWFPLKTRACCEACANLKGAFLVAV 253

☐ >gi|7024415|emb|CAB75882.1| sucrose transporter 1 [Hordeum vulgare subsp. vulgar]
 Length = 523

Score = 330 bits (772), Expect = 7e-89

Identities = 223/685 (32%), Positives = 253/685 (36%), Gaps = 408/685 (59%)

Query: 46 ELSAGV-----VDHVAPISLG-----MVAGGVQYGW-----LTPYVQTLGLG 82
 ELS GV + ISLG MVAGGVQYGW LTPYVQTLGL
 Sbjct: 11 ELSVGVGGGGGAAPRAAEPAVQISLGRILLAGMVAGGVQYGWALQLSLLTPYVQTLGLS 70

Query: 83 -PIAGDRCTSFMWLC-----VGLYS-----PFILTGCMLIIGAAHGPR 119
 + TSEFMWLC VGLYS PFILTGC+LI
 Sbjct: 71 HAL-----TSEFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRRRPFILTGCVLI----- 117

Query: 120 WLLDFSMADLCFCSSTNNWWETCCEAVFLVLVPYRAEVETECVAVIVDTKE---L--G-- 172
 C AV ++V + A++ A + D+KE L G
 Sbjct: 118 -----CLAV--IIVGFSADIG---AALGDSKEECSLYHGPR 148

Query: 173 -HAAIVY-----NNTVQG-----D---HHGPSA-----LGNIL----- 196
 HAAIVY NNTVQG D HGPSA LGNIL
 Sbjct: 149 WHAAIVYVLGFWLLDFSNNNTVQGPALMADLSAQHGPSAANSIFCSWMALGNILGYSSG 208

Query: 197 -----KWFPFVGFSDDHCSLYVLGFWPARAMA-----ANSIGYSSGLKTS AFLVAV--- 242
 KWFPF+ R A AN LK AFLVAV
 Sbjct: 209 STNNWHKWFPL-----RTRACCEACAN-----LK-GAFLVAVLFL 243

Query: 243 -----IFAKE-----ANLKGACLTVTNLNENLPTTKAGG-----PTGPLALAVLK-- 281
 IFAKE A LP TKA G PTGP LAV K
 Sbjct: 244 SLALVITLIFAKEVPYKAIA-----PLP-TKANGQVEVEPTGP--LAVFKGF 287

Query: 282 -----MPSVLLVT-----FFFIYDTHGDPKLYSNAGFKDLPPAITWLSWWMGREI 328
 MPSVLLVT FFFIYDTH WMGREI
 Sbjct: 288 KNLPPGMPSVLLVTGLTWLSWFFFIYDTH-----WMGREI 323

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Query: 329 Y-----QISAFNE-----LLNSVIL-----PMCRKVG-----FMV 355
          Y      + +AF E      LLLNSV+L      PMC+++GP      +V
Sbjct: 324 YHGDPKGTPAEANAFOEGVRAGAFGLLLNSVVLGFSSFLIEPMCKRLGPRVWVSSNMLV 383

Query: 356 CVAMASLRDYHGYSIKAVCSVGVRVGAFGGFSSFLIERVVVWTSNISFW----- 404
          C++MA      A+C      I      IS+W
Sbjct: 384 CLSMA-----AIC-----I-----ISWWATQDLHGYIQH 407

Query: 405 -ITAN-----AFLGVPTAQLAATALVQDAVLFA-PFAV-----GLCT 439
          ITA+      AFLG+P L      A+L++ PFAV      GLCT
Sbjct: 408 AITASKEIKAVSLALFAFLGIP---L-----AILYSVPFAVTAQLAANKGGQGLCT 456

Query: 440 GVLNIATRGGGQSIVIPQVIIAL-----NIPAF-----VVGVFVAVSA 476
          GVLNIA      IVIPQVIIA+      NIPAF      VVG+F
Sbjct: 457 GVLNIA-----IVIPQVIIAVGAGPWDELFGKGNIPAFGMASVFALIGGVVGIF---- 505

Query: 477 GGGVASALLPKIGHFALVGSKRQFR 501
          LLPKI      S+RQFR
Sbjct: 506 -----LLPKI-----SRRQFR 516

```

Score = 59.6 bits (133), Expect = 3e-07

Identities = 39/107 (36%), Positives = 39/107 (36%), Gaps = 66/107 (61%)

```

Query: 1 MARGDGRG-----AA--AV-----RLILAG-----ALQLSL- 24
          MARG G G      AA AV      RLILAG      ALQLSL
Sbjct: 1 MARGGGNGEVELSVGVGGGGGAAPRAEPAVQISLGRILLAGMVAGGVQYGWALQLSLL 60

Query: 25 -----SHALTS-----VVQP---L-----RWGRRR 41
          SHALTS      VVQP L      RWGRRR
Sbjct: 61 TPYVQTLGLSHALTSFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRRR 107

```

☐ >gi|20152871|gb|AAM13408.1| sucrose transporter SUT1A [Triticum aestivum]
Length = 522

Score = 303 bits (709), Expect = 8e-81

Identities = 219/698 (31%), Positives = 244/698 (34%), Gaps = 435/698 (62%)

```

Query: 46 ELSAGV-----VDHVAPISLG-----MVAGGVQYGW-----LTPYVQTL 79
          ELS GV      VD ISLG      MVAGGVQYGW      LTPYVQTL
Sbjct: 11 ELSVGVGAGAGAGADAPAVD---ISLGRILLAGMVAGGVQYGWALQLSLLTPYVQTL 66

Query: 80 GLG-PIAGDRCTSFMWLC-----VGLYS-----PFILTCMLIIGA AH 116
          GL +      TSFMWLC      VGLYS      PFILTC+LI
Sbjct: 67 GLSHAL-----TSFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRRRPFILTCILI----- 116

Query: 117 GPRWLLDFSMADLCFCSSTNNWWETCCEAVFLVLPYRAEVETECVAVIVDTKE---L-- 171
          C AV V+V + A++      A + D+KE L
Sbjct: 117 -----CIAV--VVVGFSADIG---AALGDSKEECSLYH 144

Query: 172 G---HAAIVYNNTVQGDHGHGPSALGNILKWFPFVGSSDHCSLYVLGFW----- 217
          G HAAIV      YVLGFW
Sbjct: 145 GPRWHAAIV-----YVLGFWLLDFSNNTVQG 170

Query: 218 PARA-MA-----ANSI-----GYSSG-----LKT----- 235
          PARA MA      ANSI      GYSSG      L+T

```

Sbjct: 171 PARALMADLSAQHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLRTRACCEACAN 230

Query: 236 --SAFLVAVIFAKEANLKGA-CLTVTL---NEN-----LPTTKAGG-----PTGPLAL 277
 AFLVAV+F L A CL +T+ E LPT KA G PTGPLA

Sbjct: 231 LKGAFLVAVLF-----L--AFCLVITVIFAKEIPYKAIAPLPT-KANGQVEVEPTGPLA- 281

Query: 278 AVLKMPSVLLVTFPFILYDTHGDPKLYSNAGFKDLPPAI-----TWLSW----- 322
 V K GFK+LPP + TWLSW

Sbjct: 282 -VFK-----GFKNLPPGMPSVLLVTGLTWLSWFPFILI 313

Query: 323 ---WMGREIYQISAFNELLLNSVILPMCRKVGPFMVCVAMASLRDYHG-----YSI 370
 WMGREI YHG +

Sbjct: 314 DTDWMGREI-----YHGDPKGTPEANAF 337

Query: 371 KAVCSVGVRVGAFG-----GFSSFLIE-----RVVWVTSN-----IS 402
 +A GVR GAFG GFSSFLIE RVVWV+SN IS

Sbjct: 338 QA----GVRAGAFGLLLNSVVLGFSSFLIEPLCKRLGPRVWVSSNFLVCLSMACIIS 393

Query: 403 FW-----ITAN-----AFLGVPTAQLAATALVQDAVLFA-PFAV--- 435
 +W ITA+ AFLG+P L A+L++ PFAV

Sbjct: 394 WWATQDLHGYYQHAIASKEIKIVSLALFAFLGIP-----L---AILYSVPFAVTAQ 442

Query: 436 -----GLCTGVLNIATRGGGQSIVIPQVIIAL-----NIPAFVVGVFVAV 474
 GLCTGVLNIA IVIPQVIIA+ NIPAF

Sbjct: 443 LAANRGGGQGLCTGVLNIA-----IVIPQVIIAVGAGPWDELFKGKNIPAF----- 488

Query: 475 SAGGGVASA-----LLPKIGHFALVGSKRQFR 501
 GVASA LLPKI S+RQFR

Sbjct: 489 ----GVASAFALIGGIVGIFLLPKI-----SRRQFR 515

Score = 60.4 bits (135), Expect = 2e-07

Identities = 38/106 (35%), Positives = 38/106 (35%), Gaps = 65/106 (61%)

Query: 1 MARGDGRG-----AAAV-----RLILAG-----ALQLSL-- 24
 MARG G G A AV RLILAG ALQLSL

Sbjct: 1 MARGGGNGEVELSVGVGGGAGAGGADAPAVDISLGRRLILAGMVAGGVQYGWALQLSLLT 60

Query: 25 -----SHALTS-----VVQP---L-----RWGRRR 41
 SHALTS VVQP L RWGRRR

Sbjct: 61 PYVQTLGLSHALTSFMWLCGPAGLVVQPCVGLYSDKCTSRWGRRR 106

☐ >gi|19548165|gb|AAL90455.1| sucrose transporter SUT1D [Triticum aestivum]
 gi|20152875|gb|AAM13410.1| sucrose transporter SUT1D [Triticum aestivum]
 Length = 523

Score = 301 bits (703), Expect = 5e-80

Identities = 217/699 (31%), Positives = 244/699 (34%), Gaps = 436/699 (62%)

Query: 46 ELSAGV-----VDHVAPISLG-----MVAGGVQYGW-----LTPYVQT 78
 ELS GV VD ISLG MVAGGVQYGW LTPYVQT

Sbjct: 11 ELSVGVGGGGGAAGGGEQPAVD----ISLGRRLILAGMVAGGVQYGWALQLSLLTPYVQT 66

Query: 79 LGLG-PIAGDRCTSFMWLC-----VGLYS-----PFILTCMLIIGAA 115
 LGL + TSFMWLC VGLYS PFILTC+LI

Sbjct: 67 LGLSHAL-----TSFMWLCGPAGLVVQPCVGLYSDKCTSRWGRRRPFILTCILII---- 117



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

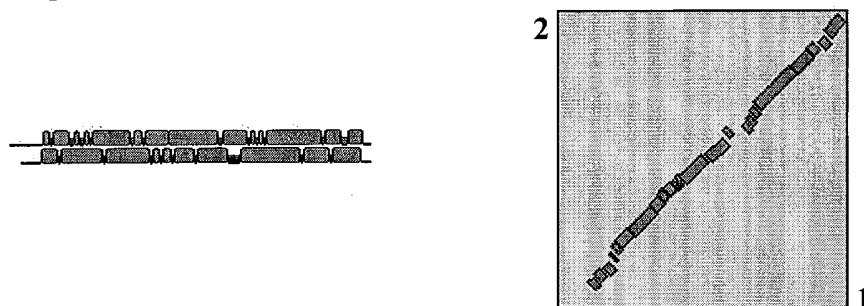
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.00000** wordsize: **3** Filter ☒ Align

Sequence 1 lc|seq_1 Length 501 (1 .. 501)

Sequence 2 lc|seq_2 Length 510 (1 .. 510)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 42.0 bits (97), Expect = 0.066

Identities = 115/512 (22%), Positives = 182/512 (35%), Gaps = 143/512 (27%)

```

Query: 62  VAGGVQYGW-----LTPYVQTLGLGPIAGDRCTSFMWLC-----VGLYS---- 100
      +A GVQ+GW      LTPYVQ LG+      +   ++WLC      VG YS
Sbjct: 40  IAAGVQFGWALQLSLLTPYVQLLGIP----HKWAAIWLCPISGMLVQPIVGYYSDRCQ 95

Query: 101 -----PFILTG--CMLIIGAAHGPRWLLDFSMADLCFCSSTNNWWEETCCEAVFLVLV 151
      PFI +G C+ I      G      + +      D      + T      T      F +L
Sbjct: 96  SSFGRRRPFIASGAGCVAISVILIGFAADIGYKAGD--DMNKTLPRAVTVFVIGFWILD 153

Query: 152 PYRAEVETECVAIVD-----TKELGHAAIVYN-----NTVQGDHHGPSALGNILKWFPF 201
      ++ C A++ D      T+ + A +Y      + G+ G + N+ K FPF
Sbjct: 154 VANNMLQGPCRALLDLCNGDTRMRSANALYRFFMAVGNILGNAAG--SYNNLYKLFPF 211

Query: 202 VGFSSDH-CSLYVLGFWPARAMAANSIGYSSGLKTS AFLVAVIFAKEANLKGACLTVTLN 260
      S H C LY      A + I      + +      + V+ K+ + A      +
Sbjct: 212 ---SKTHACDLYC-----ANLKSCFIISIVLLIFITVLALT VVREKQWSPDEA-----D 257

Query: 261 ENLPPTKAGGPTGPLALAVLKMPSVLLVT-----FPFILD TDHGD PKLYSNAG 309
      E P++      G L A+ +P +L+      FPFIL+DTD
Sbjct: 258 EEPSSGKIPVFGELLRALKDLPRLMLLAVTCLNWIWF PFILFDTD----- 306

Query: 310 FKDLPPAITWLSWWMGREIY-----QISAFNE-----LLLNSV-----ILPMCRK 349
      WMGREIY      Q      +++      LLLNSV      + + R
Sbjct: 307 -----WMGREIYGGTAGQGKLYDQGV RVVGS LGLLLNSV VGLT SI AVEY LVRG 353

Query: 350 VGPFMVCVAMASLRDYGYSIKAVCSVGVRVGAFFGFSFLIERVVWVTSNISFWITANA 409
      VG      +      +      +      G + V S      +      G + L+      +S +      +

```

SEQ ID NO: 2
GI 4091871

Sbjct: 354 VGGVKILWGLVNFLLAIGLVMTVVVSKVAQHQRQHGANGQLLPPSAVKAGALSLF-----S 409

Query: 410 FLGVPTAQLAATALVQDAVLFAFPAV--GLCTGVLNIATRGGGQSIVIPQVIIAL----- 462
LG+P + + ++ + GL GVLN+A IV+PQ+I+++

Sbjct: 410 ILGIPLSITFSIPFALASIYSSGSGAGQGLSLGVLNLA-----IVVPQMIVSVLAGPF 462

Query: 463 -----NIPXXXXXXXXXXXXXXXXXXLLPK 487
N+P LLPK

Sbjct: 463 DSLFGGGNLPAFVVGAISSAISGVLAIVLLPK 494

CPU time: 0.35 user secs. 0.05 sys. secs 0.40 total secs.

Lambda	K	H
0.325	0.140	0.450

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 2284

Number of Sequences: 0

Number of extensions: 222

Number of successful extensions: 5

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 0

Number of HSP's successfully gapped in prelim test: 1

Number of HSP's that attempted gapping in prelim test: 1

Number of HSP's gapped (non-prelim): 1

length of query: 501

length of database: 776,568,843

effective HSP length: 135

effective length of query: 366

effective length of database: 776,568,708

effective search space: 284224147128

effective search space used: 284224147128

T: 9

A: 40

X1: 15 (7.0 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 40 (21.6 bits)

S2: 79 (35.0 bits)